dest.

ESULT 4 AF51541

AAF51541 standard; DNA; 15

IGF-I oligonucleotide #2501.

IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; neovascular condition of the retina; ss.

Homo sapiens.

WO200078341-A1

28-DEC-2000.

21-JUN-2000; 2000WO-AU000693

21-JUN-1999; 99US-0140345P

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight S, Werther GA, Edmondson SR;

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 77; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an cantisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 creceptor, IGF binding protein [IGFBP]-2 or IGFBB3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, confidential of the factor mediated cell proliferation, confidential of the present sequence is an coligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-C oligonucleotide of the present invention (see AAF45151 and AAF45153-C oligonucleotide of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of the present invention (see AAF45151 and AAF45153-C oligonucleotides of see AAF45151 and AAF45153-C oligonucleotides of see AAF45151 and AAF45153-C oligonucleotides of see AAF45151 and AAF45153-C olig or any other hyperplasia

Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Matches Query Match Local Similarity 7; Conserv Conservative 100.0%; 6, Pred. No. 1.8; Score 13; Mismatches DB 1; Length 15; 0; Indels 0, Gaps

CUUCGUCUUUGCA 13

ESULT 5

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityrlasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; 30-MAR-2001 AAF51543 AAF51543 standard; DNA; 15 neovascular condition of the retina; ss. IGF-I oligonucleotide #2503. (first entry)

Homo sapiens.

WO200078341-A1

28-DEC-2000.

21-JUN-2000; 2000WO-AU000693.

21-JUN-1999; 99US-0140345P

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

Example 8; Page 77; 201pp; English.

skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-like Growth Factor [IGP]-1 receptor, IGP binding protein [IGPBP]-2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pllaris, serborrhoea, keloids, keratosis, hyperneovascular condition of the retina, byperneovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood disease, kidney disease, hyperproliferation of the inside of blood The present invention relates to a method for ameliorating the effects of or any other hyperplasia

Sequence 15 BP; 2 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Matches Query Match Best Local Similarity Conservative 50.0%; 6 Score 12; DB Pred. No. 2.5; Mismatches DB 1; Length 15; <u>,</u> Indels 0,

Gaps

0

밁 S 2 uucgucuuugca 13 TICGICITIGCA 12

0

RESULT 6

AAF51539 standard; DNA; 15 BP

AAF51539;

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ALIGNMENTS

Hepatitis B virus

## Copyright GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd

OM nucleic - nucleic search, using sw model

September 1, 2006, 12:04:34; Search time 0.001 Seconds (without alignments) 9.490 Million cell updates/sec

Title: Perfect score: us-09-847-601b-88 13

cuucgucuuugca 13

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 0

Searched: 34 seqs, 365 residues

Total number of hits satisfying chosen parameters:

Minimum Maximum DB DB seq length: 5
seq length: 80

Post-processing: Minimum Match Maximum Match Match 0 100%

Listing 34 summaries

Database :

and is derived by analysis of the total Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being p score distribution being printed

## SUMMARIES

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ABZ72849; ABZ72849 standard; RNA; 13 BP 09-APR-2003 (first entry)

Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; macular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss

IGF1 Rz1 ribozyme target sequence SEQ ID NO:88

Synthetic.

WO200288320-A2.

07-NOV-2002.

01-MAY-2002; 2002WO-US013679

01-MAY-2001; 2001US-00847601.

(UYFL ) UNIV FLORIDA.

Lewin æ, Shaw LC, Grant ă

WPI; 2003-111880/10.

A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.

Claim 1; Page 80; 115pp; English.

RESULT 1
ABZ72849
ID ABZ72849
ID ABZ72849
ID ABZ72849
ID ABZ7
XX ABZ7
XX ABZ7
XX Hair
XX Hair
XX Opht
XX Opht
XX Opht
XX Opht
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XX OP-A
XX OP-A CC (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a CC first ribozyme that specifically cleaves an mRNA encoding a protein, CC polypeptide, or peptide selected from the group of rod opsin, iNOS, CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a CC vector comprising a polymucleotide encoding the ribozyme, where the CC polymucleotide operably positioned downstream of at least a first CC promoter that directs expression of the polymucleotide in a selected CC comprising the ribozyme or the polymucleotide; (d) an AAV vector CC comprising the ribozyme or the polymucleotide; (d) an AAV vector CC comprising the ribozyme or the polymucleotide. Also described is a method CC for decreasing the amount of mRNA encoding a selected polypeptide in a CC retinal cell of a mammalian eye, comprising providing to the eye the CC composition described above, and for a time effective to specifically CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or retinal CC dysfunction, (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant condition, e.g. atrophic or pigmented lesions of the eye blindness, a reduction in central or peripheral vision, or a reduction in tentral or peripheral vision, or a reduction in the creating of the eye. exemplification The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a of the present invention

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RESULT 2
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                                                 The present invention relates to a method for ameliorating the effects of Skin disorders. The method comprises contacting the skin with an cantisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing-growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an coligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAP45151 and AAF45153-19401). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, of brain or skin, growth factor-mediated malignancies, other selerotic disease, kidney disease, hyperproliferation of the inside of blood or vessels or any other hyperplasia
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Matches 13
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8;
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Query Match

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RESULT 3
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ADP
                                                                                                                                                                                     cc skin disorders. The method comprises contacting the skin with an cc antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 creceptor, IGF binding protein [IGFB]-2 or IGFBP]3, which is capable of inhibiting or reducing growth factor mediated cell proliferation, cc inflammation and/or other disorders. The present sequence is an coligonucleotide which can be used to design the antisense coligonucleotide which can be used to design the antisense coligonucleotides of the present invention (see AAF45151 and AAF45153-CC eithhyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, conceptasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complasias, scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin, a complastic scleroderma, warts, benign growths, cancers of the skin and the complastic scleroderma, warts, benign growths, cancers of the skin and the complastic sclero
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                                                                                                                          Sequence
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100.0%; Score 13; 53.8%; Pred. No. 1
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                                                                                                                                                                                                                                                                          Sequence 15
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DT 23-MAR
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skin disorder; Insulin-like Growth ractur, a receptor, ortalis; pilaris; IGP binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; kratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                         skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor. IGF binding protein [IGFBH]-2 or IGFBB), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the effects of psoriasis, ref45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
   Yeast NORF
                                        23-MAR-2001
                                                                                                               AAF38544 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for ameliorating the effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; Page 77; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-041421/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGF-I oligonucleotide #2499
                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                      6.
                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                               cuuceucuuuec 12
   gene SAGE tag oligonucleotide
                                                                                                                                                                                                                                                                                                                                                            BP; 2 A;
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Werther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                        (first entry)
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                                                                                                                                                                                                                                                                                                      92.3%;
                                                                                                                                                                                                                                                                                                                                                            5 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edmondson SR
                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                      Score 12; DB 1; Length 15
Pred. No. 2.5;
     SEQ ID NO:5283
                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Off.
                                                                                                                                                                                                                                                                                    0
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RESULT 8
AAF41570
ID AAF4
XX
AC AAF4
XX

AAF41570 standard; DNA;

10 ВP

AAF41570;

맑 S

10

1 cuncencum 10

Query Match Best Local Matches

4. Similarity

Conservative

6

Mismatches

<u>,,</u>

Indels

0;

Gaps

0

40.0%;

Score 10; DB 1; Length 10; Pred. No. 7.7;

Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression varies by at cleast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human plan with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression in a cycle study, monitor and affect phases of the cell cycle, the differentially cycle and for identify candidate drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle. The method was a condidate drugs which affect the cell cycle. The method was a condidate drugs and condidate drugs which affect the cell cycle in the exemplification of the present invention.

Candidate drugs used in the exemplification of the present invention.

ARF33262 to ARF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast gene coding sequences comprising NORF genes with serial analysis gene expression (SAGE) tags, useful for studying, monitoring and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 188; 419pp; English.
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23-MAR-2001 (first entry)

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The present invention describes an isolated DNA molecule comprising a CC coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamotated ORP) genes CC comprising a SAGE (serial analysis of gene expression) tag. Also CC described are: (1) a method (M1) of using NORF genes to affect the cell Cycle comprising administering a NORF gene whose expression varies by at CC phase, S phase and G2/M; (2) a method (M2) for screening candidate CC antifungal drugs comprising: (a) contacting a test substance with a yeast CC varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M2) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression CC contiguous nucleotides of a NORF gene whose expression varies as in M1; (2) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a CC yeast cell comprising contacting a yeast cell with a candidate drug and contacting a pression in the yeast cell of at least 1 NORF gene may be used to study, monitor and affect phases of the cell cycle, the differentially cycle and for identification of the cycle, the differentially cycle and for identification of antifungal drugs. AAF33261 to AAF33267 represent 1inkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
                                     Query Match
Best Local S
Matches 4
                                                                                                                   Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast gene coding sequences comprising NORF genes with serial analysis gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200077214-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORP; nor previously assigned open reading frame; nonannotated ORF; SAGE; nor previously assigned open reading frame; nonannotated ORF; SAGE; nor previously assigned open expression; antifungal; tag; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 296; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS.
                                                          Local Similarity
1 CUUCGUCUU 9
                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00335032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d8.
                                                        69.2%;
                                                        Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinzler
                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      日
                                                                           Length 10;
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                                   0;
                                     Gaps
                                     0
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RESULT 9
AAF35016
ID AAF3

AAF35016 standard; DNA; 10 BP

S 片

2 uuccucuuu 10

Matches

Similarity

69.2**%**; 33.3**%**;

Score 9; Pred. No.

DB 1;

Length 10;

Conservative

6.

Mismatches

0,

0,

Gaps

0

Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

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The present invention describes an isolated DNA molecule comprising a CC coding sequence of a yeast gene selected from a group of 745 NORF (not CC previously assigned open reading frame; or nonamnotated ORP) genes CC comprising a SAGE (serial analysis of gene expression) tag. Also CC comprising a SAGE (serial analysis of gene expression) tag. Also CC described are: (1) a method (M1) of using NORF genes to affect the cell CC cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log CC phase, S phase and G2/M; (2) a method (M2) for screening candidate CC cell; and (b) monitoring expression of a NORF gene whose expression of CC varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 comprising contacting a whose expression varies as in M1; and (b) munan genes which are involved in cell cycle progression in a CC contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a CC class of drugs having a characteristic effect on gene expression in a CC contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression varies as in M1; and the properties of a contiguous nucleotides of a NORF gene whose expression varies as in M1; and the control of a contiguous nucleotides of a NORF gene whose expression varies as in M1; and the properties of a contiguous nucleotides of a NORF gene whose expression varies as in M1; and the properties of a contiguous nucleotides of a NORF gene whose expression varies as member of a contiguous nucleotides of a NORF gene whose expression varies as in M1; and the properties of a contiguous nucleotides of a NORF gene hose of a NORF gene whose expression is a ffected by the class of drugs. The NORF gene whose expression is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast
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AAF35467
ID AAF35
XX AAF35
XX Yeast
XX Yeast
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                                                                                                                                                                          CC comprising a SAGE (a) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log CC phase, S phase and G2/M; (2) a method (M2) for screening candidate CC antifungal drugs comprising: (a) contacting a test substance with a yeast CC cell; and (b) monitoring expression of a NORF gene whose expression of CC varies as in M1, where a test substance which modifies the expression CC comprising contacting and test substance which modifies the expression CC comprising contacting human panes which are involved in cell cycle progression of CC comprising contacting human DNA with a probe which comprises at least 10 CC contiguous nucleotides of a NORF gene whose expression varies as in M1; CC and (4) a method (M4) for identifying a candidate drug as a member of a CC varies of drugs having a characteristic effect on gene expression in a CC value of drugs having a contacting a yeast cell with a candidate drug and CC monitoring expression in the yeast cell of the a candidate drug and cc expressed genes may be used to identify candidate drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle. The CC expressed genes may be used as markers of phases of the cell cycle. The CC cycle and for identification of antifungs. AAF3358 to AAF44064 CC represent SACE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE companies and the present invention.
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes
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                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nor previously assigned open reading serial analysis of gene expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast NORF gene SAGE tag oligonucleotide
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                              Local
Similarity
4; Conserv
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                                                                                                                              B₽;
   Conservative
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                                                                                                                              <u>و</u>
                              Score 9;
Pred. No.
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                                                                                                                              5 T;
   Mismatches
                                                                                                                              0 U; 0 Other;
                                                             DB 1; Length 10;
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   Indels
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RESULT 11
AAF34844/c
ID AAF3488
XX AAF3488
XX Yeast
XX Yeast
XX Yeast
XX Yeast
XX Yeast
XX WO2000
XX Iinker
XX Iinc
PP 14-JUN
XX UYJO
PI Velcul
XX Yeast
PT Gene (
CC Compri
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                                                            The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not coding sequence of a yeast gene selected from a group of 745 NORF (not comprising assigned open reading frame; or monannotated ORF) genees comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression varies by at CC cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate CC cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (a) a method (M3) for cell cycle progression of cc comprising contacting human bun with a probe which modifies the expression of contiguous mucleotides of a NORF gene whose expression varies as in M1; and (b) munan genes which are involved in cell cycle progression of cc contiguous mucleotides of a NORF gene whose expression varies as in M1; and class of drugs having a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expressed genes may be used as markers of phases of the cell cycle. The ceptes and for identification of antifungal drugs. AAF33268 to AAF34064 crepressent SAGE tags used in the exemplification of the present invention.

CC method, in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001
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Best Local

l Similarity 4; Conserva

44.48; 69.2%;

; Score 9; DB 1; Pred. No. 11; 5; Mismatches

DB 1;

Length 10; 0

Indels

0

Gaps

0

Sequence 10

BP; 6

A; 1 C; 3 G; 0 T; 0 U; 0 Other;

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0

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RESULT 12
AAF34839/c
ID AAF348
The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not C coding sequence of a yeast gene selected from a group of 745 NORF (not C coding sequence of a yeast gene expression) tag. Also comprising a SAGE (serial analysis of gene expression) tag. Also coccept comprising administering a NORF gene whose expression varies by at C least 10% between any two phases of the cell cycle selected from log cycle comprising administering a NORF gene whose expression of antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contriguous nucleotides of a NORF gene whose expression of contiguous nucleotides of a NORF gene whose expression of contiguous nucleotides of a NORF gene whose expression in a candidate antifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of a teat 1 NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a control of antification of the sell cycle, the differentially expressed genes may be used to study, monitor and affect phases of the cell cycle, the differentially cycle and for identification of antifungal drugs which affect the cell cycle. The cycle and for identification of antifungal drugs which affect the cell cycle. The method in the present invention.

CC methods in the present linkers and PCR primers used in the SAGE method. In the SAGE in the AFA33267 represent shows the comprision of the present invention.
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Sequence 10
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exemplification of the present invention

ARESULT 13
AAF42946
ID AAF42
XX AAF422
XX AAF42
XX AAF42
XX AAF42
XX Yeast
XX Yeast
XX Yeast
XX WO200
XX Sacch
XX 11-JU
XX 11-JU
XX 11-JU
XX 16-JU
XX 16-JU
XX PF 14-JU
XX PF Ś 닭 Matches Best Local Query Match Yeast gene coding sequences comprising NORF genes with serial analysis gene expression (SAGE) tags, useful for studying, monitoring and WPI; 2001-061874/07. Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; SAGE; AAF42946 standard; DNA; Velculescu V, 14-JUN-2000; 2000WO-US016223 WO200077214-A2. Saccharomyces cerevisiae. linker; PCR primer; nor previously assigned open reading frame; non serial analysis of gene expression; antifungal; 23-MAR-2001 AAF42946 (UYJO ) UNIV JOHNS HOPKINS. NORF gene SAGE 10 CTTCTTCTTT 1 1 COUCGUCUUU 10 Similarity Conservative (first entry) Vogelstein B, 99US-00335032 ds. 64.6%; 30.0%; tag oligonucleotide SEQ 10 ВP Score 8.4; Pred. No. 1 Kinzler K; Mismatches 13; ᇤ 1; ID NO:11085 Length 10 tag; identification Indels <u>,</u> Gaps

affecting phases of the cell O.

Example; Page 345; 419pp; English.

CC comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate CC cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) munan genes which are involved in cell cycle progression of cell; and (b) munan genes which are involved in cell cycle progression of cell; and (b) munan genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; and (d) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cell comprising contacting a yeast cell with a candidate drug and cell comprision contacting a yeast cell with a candidate drug and cell comprises of an other cell of the least 10 NORF genes may be used to study, monitor and affect phases of the cell cycle. The cell cycle and for identifycation of the cell cycle, the differentially certained to the cell cycle and for identification of antifungal drugs. AAF33268 to AAF33267 represent linkers and PCR primers used in the SAGE centbod, in the exemplification of the present invention. The present invention describes an isolated DNA molecule comprising coding sequence of a yeast gene selected from a group of 745 NORF (previously assigned open reading frame; or nonannotated ORF) genes not)

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AAF42256/c
IID AAF4225
XI AAF422
XI Yeast
XI Yeast
XI WO2000
XI WO2000
XI WO2000
XI UV-LCU
XI WO2000
XI VELCU
XI VELCU
XI Yeast
PH Gene (
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Cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate CC antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of CC varies as in M1, where a test substance which modifies the expression of CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for CC comprising contacting human DNA with a probe which comprises at least 10 CC contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a CC class of drugs having a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug be used to study, monitor and affect phases of the cell cycle, the differentially contacting as markers of phases of the cell cycle. The control cycle cycle and for identification of antifungal drugs which affect the cell cycle.
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The present invention describes an isolated DNA molecule comprising a CC coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes CC comprising a SAGE (serial analysis of gene expression) tag. Also CC described are: (1) a method (M1) of using NORF genes to affect the cell CC cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log CC phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast CC cali; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for dentifying human genes which are involved in cell cycle progression cC contiguous mucleotides of a NORF gene whose expression in CC contiguous mucleotides of a NORF gene whose expression varies as in M1; candidate drugs a member of a CC class of drugs having a characteristic effect on gene expression in a CC yeast cell comprising contacting a yeast cell with a candidate drug as a member of a CC yeast cell comprising contacting a yeast cell with a candidate drug as a member of a characteristic effect on gene expression in a probe which comprises at least 10 comprises of a force of the cell cycle, the differentially be used contacting a proper cell of at least 10 NORF genes whose expression in a fafected by the class of drugs. The NORF genes may be used contacting the proper cell cycle, the differentially
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a conditate drug and contacting a yeast cell with a candidate drug and
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also conscribed are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at CC cycle comprising administering a NORF gene whose expression varies by at CC elast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast CC eal; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting and contacting human DNA with a probe which comprises as in M1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast gene coding sequences comprising NORF genes with serial analysis gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF, nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 188; 419pp; English.
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for
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                                                     comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. ARF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33261 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying human genes which are involved in cell cycle progression
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                   Conservative
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11
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30.0%;
                  6
                           Score 8.4; D
Pred. No. 13;
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RESULT 19
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 24-SEP-2002
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                                          ABK96059 standard; DNA; 10
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Human; lipase; hormone sensitive; Human LIPE polymorphism; primer; ss. gene polymorphism detection oligonucleotide primer #34. LIPE; isogene; obesity; male sterility;

Homo sapiens

WO200240502-A2.

23-MAY-2002

16-NOV-2001; 2001WO-US043518

16-NOV-2000; 2000US-0249302P

GENAISSANCE PHARM INC

Anastasio AB, Bentivegna SC, Chew A, Koshy B, Rounds Ħ

WPI; 2002-519369/55

Novel improving efficiency and diseases associated with genetic variants of Lipase, Hormone-Sensitive isogenes, useful for ving efficiency and reliability in drug development for treating ses associated with LIPE activity, e.g. obesity and male sterility.

Claim 17; Page 16; 142pp; English

nucleotide sequence which comprises lipase, hormone sensitive (LIPE) isogenes. The invention is useful in screening for drugs targeting LIPE isogenes that are useful for treating obsestly and male sterility. The methods of the invention are useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with LIPE activity. The polynucleotide is useful in studying the expression and function of LIPE, and in expressing LIPE protein for use in screening for candidate drugs to treat diseases related to LIPE activity. It is also useful in studying the effect of the variation on the biological activity of LIPE as well as on The present invention relates to a new polynucleotide comprising a nucleotide sequence which comprises lipase, hormone sensitive (LIPE)

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RESULT 20
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Matches 4
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                     The present invention describes the use of tumour endothelial marker (TEM) proteins for identifying a ligand involved in endothelial cell regulation, inhibiting neoangiogenesis, screening for neoangiogenesis, promoting neoangiogenesis, identifying candidate drugs for treating tumours or promoting wound healing or identifying endothelial cells. Also described: (1) identification of a ligand involved in endothelial cell regulation; (2) inhibiting neoangiogenesis; (3) promoting neoangiogenesis in a patient; (4) screening for neoangiogenesis in a patient; (5) inhibiting neoangiogenesis in a patient; (6) identifying endothelial cell regulation; condidate drugs for treating tumours or promoting wound healing; and (6) identifying endothelial cells. TEM proteins have cytostatic and vulnerary activities. The TEM proteins are useful for identifying a ligand involved in endothelial cell regulation, inhibiting neoangiogenesis, screening for neoangiogenesis, promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the binding affinity of candidate drugs targeting LIPE for the treatment of obesity and male sterility. The invention is useful for studying the expression of LIPE isogenes in vivo, for in vivo screening and testing of drugs targeted against LIPE protein, and for testing the efficacy of therapeutic agents and compounds for treating obesity and male sterility in a biological system. The present nucleic acid sequence represents one of a collection (ARE96026-ARE96083) of oligonucleotide primers that were used in the invention to detect polymorphisms in the human LIPE gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    St Croix B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002; 2002US-0393023P
01-APR-2003; 2003US-0458964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoangiogenesis inhibition; neoangiogenesis neoangiogenesis promotion; neoangiogenesis; cytostatic; vulnerary; human; standard tag;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   candidate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor endothelial marker proteins for inhibiting neoangiogenesis, ing for neoangiogenesis, promoting neoangiogenesis, identifying area arms for treating tumors or promoting wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 101; 113pp; English
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Pred. No. 13;
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treating tumours
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RESULT 21
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                                                                                                                                              This invention relates to a novel analyte detection device, having several sensing elements, where one or more probes are coupled to each of the sensing elements, and where at least one of the probes is configured to interact with an analyte, and where at least one sensing element produces a signal when the analyte interacts with a probe, and where sensing elements produce detectable signals in predetermined pattern that represents a code that identifies analyte. The invention is useful for
                                                                                                analyzing analytes such as DNA, RNA, proteins, enzymes, oligopeptides, antigens, antibodies or organic molecules. The present sequence is the of an oligonucleotide probe which targets a region of the human p53 ge and which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                 Analyte detection device, has sensing elements coupled with are capable of producing signal when analyte interacts with determining identity of analyte based on signal produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoting wound healing or identifying endothelial cells. The present sequence represents a cytoplasmic tumour endothelial marker standard oligonucleotide, which is used in the exemplification of the present
                                                                           Sequence 10
                                                                                                                                                                                                                                               Example;
                                                                                                                                                                                                                                                                                                                                                          Schmid
                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2003; 2003US-0465336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                            Similarity 4; Conser
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                                                                           A; 2 C; 3
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Matches 3
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                                                                                                                                                         the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
                                                                                                                                                        Sequence 10 BP; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts BL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metastatic breast tumour cell upregulated transcript tag #1289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1999;
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       N
                                                   Similarity
3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHANKARA S.
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shankara
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                                                                                                                                                     A; 1 C; 3 G; 1 T; 0 U; 0 Other;
                                                                             61.5%;
37.5%;
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                                                        <u>ب</u>
                                                                             Score 8;
Pred. No.
                                                           Mismatches
                                                                                DB 1;
15;
                                                                                                  Length 10;
                                                        <u>,</u>
                                                        Indels
                                                      <u>,</u>
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                                                        Gaps
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ARESULT 24
AAF34140/c
ID AAF341
XX AAF341
XX AAF341
XX CAF541
XX C
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AAH63934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular
                                                                                                                                                   Yeast NORF
                                                                                                                                                                                                         23-MAR-2001
                                                                                                                                                                                                                                                                  AAF34140;
                                                                                                                                                                                                                                                                                                                           AAF34140 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 56; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-367706/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ubiquitously expressed transcriptome sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2001
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                                                                                                                                             gene SAGE tag oligonucleotide SEQ ID NO:879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred.
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ARSULT 25
AAAF42583
ID AAF42
XX AAF42
XX AAF42
XX AAF42
XX AAF42
XX AAF42
XX PG AAF42
XX Yeast
XX Yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                        CC comprising a SAGEX (a) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log CC phase, S phase and G2/M; (2) a method (M2) for screening candidate CC antifungal drugs comprising: (a) contacting a test substance with a yeast CC cell; and (b) monitoring expression of a NORF gene whose expression of CC varies as in M1, where a test substance which modifies the expression CC varies as in M1, where a test substance which modifies the expression of comprising contacting human far involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 CC contiguous nucleotides of a NORF gene whose expression varies as in M1; CC and (4) a method (M4) for identifying a candidate drug as a member of a CC varies of drugs having a characteristic effect on gene expression in a CC vest cell comprising contacting a yeast cell with a candidate drug and CC expressed genes may be used as markers of phases of the cell cycle. The corresponding to the cell cycle and for identification of the cycle, the differentially corresponding to the cell cycle. The corresponding to the exemplification of the cycle of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGEX method, in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10722.
                                                                                                               AAF42583
                                                                                                                                                AAF42583 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes
                                                                          23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Velculescu V, Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 31; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        affecting phases of the cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                        Score 8;
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                                                                                                                                                                                                                                                                                                                                      8; DB 1; Length 10;
No. 15;
                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                     Gaps
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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

RESULT 26
AAF37269/c
ID AAF37269 standard; D
XX
AC AAF37269;
XX
DT 23-MAR-2001 (first
XX

DNA; 10

ВÞ

(first entry)

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w

TCTTTGCA 10

6 UCUUUGCA 13

Matches Query Match Best Local

4. Similarity

Conservative

4.

Mismatches

Indels

0;

Gaps

0;

61.5%; 50.0%;

Score 8; Pred. No.

DB 1; 15;

Length 10; ç

Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also coerribed are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human genes which are involved in cell cycle progression contacting human genes which are involved in cell cycle progression that it is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comprises at least 10 contacting human distance and least 10 contacting human distance and least 10 contacting human distance and least 10 contacting 
                                                       configuous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifumgal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORE; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;

Yeast NORF gene SAGE tag oligonucleotide SEQ

IJ

NO:4008

21-DEC-2000. WO200077214-A2 Saccharomyces cerevisiae.

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                                                                                                                                                                                                                                                                                       RESULT 27
AAF38836/c
                                                                                                                                                                                                                                                                                                               The present invention describes an isolated DNA molecule comprising a CC coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes CC comprising a SAGE (serial analysis of gene expression) tag. Also CC described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log Dhase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast CC cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a CC class of drugs having a characteristic effect on gene expression in a CC class of drugs having a characteristic effect on gene expression in a CC yeast cell comprising contacting a yeast cell with a candidate drug as a member of a CC yeast cell comprising contacting a yeast cell with a candidate drug and modern the yeast cell of at least 1 NORF gene whose expression in the yeast cell of the cell cycle. The comprise of dentification of the cell cycle, the differentially captions and the comprise of the cell cycle. The compresent SNGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                           Matches
AAF38836;
                                     AAF38836 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                       Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 143; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast gene coding sequences comprising NORF genes with serial analysis gene expression (SAGE) tags, useful for studying, monitoring and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-061874/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2000; 2000WO-US016223
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                                                                                                                                                                     6 ucuuugca 13
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                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                               61.5%;
50.0%;
                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                               Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler K;
                                                                                                                                                                                                                               DB 1; Length 10, 15;
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Gaps

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cc antifugal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression of contiguous nucleotides of a NORF gene whose expression varies as in M1; candidate of the yeast cell comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; candidate of drugs having a characteristic effect on gene expression in a comprising contacting a yeast cell with a candidate drug and contiguous nucleotides of a NORF gene whose expression in a comprising contacting a yeast cell with a candidate drug and comprising contacting a yeast cell with a candidate drug and contiguous nucleotides as markers of phases of the cell cycle. The corresponding expression in the yeast cell of at least 1 NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially capressed genes may be used as markers of phases of the cell cycle. The cethods may be used to identify candidate drugs which affect the cell cycle methods may be used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used, in the SAGE method, in the exemplification of the present invention.
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by alleast 10% between any two phases of the cell cycle selected from log phase. S phase and G2/M; (2) a method (M2) for screening candidate
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                                                                                                                                                                                                                                                    Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 199; 419pp; English.
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                                                                                                                              Local
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2 UUCGUCUU 9
                                                                                                                          Similarity
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9908-00335032
                                                                                                                      61.5%;
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                                                                                                                          Score 8;
Pred. No.
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                                                                                   Mismatches
                                                                                                                          DB 1;
15;
                                                                                                                                                                 Length 10
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Yeast NORF gene SAGE tag oligonucleotide SEQ ID

NO:8993

23-MAR-2001

(first entry

AAF42254 standard; DNA; 10 BP

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                                                                                                                                                                                                        The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression tage. Also cycle comprising administering a NORF gene whose expression varies by at CQ cycle comprising administering a NORF gene whose expression varies by at CQ phase, S phase and G2/M; (2) a method (M2) for screening candidate coll; and (b) monitoring expression of a NORF gene whose expression of comprising contacting human genes which are involved in cell cycle progression of identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression in contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression varies as in M1; contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a comprising contacting a yeast cell with a candidate drug as member of a const guous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a member of a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a member of a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a member of a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene mose expression in the yeast cell of the cell cycle. The contiguous nucleotides of a NORF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                          Sequence 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linker; PCR primer;
8
                                                                                                          Similarity
                                         GUCUUUGC 12
                                                                                                                                                                        BP; 4 A; 2 C; 2
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                                                                                                          50.0%;
                                                                                                          Score 8;
Pred. No.
                                                                                                                                                                        G; 2 T; 0 U; 0 Other;
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                                                                                                          DB 1; Length 10; 15;
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Query Match Best Local Matches

61.5%;

Score 8; Pred. No.

DB 1; Length 10; 15;

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Indels

0,

Gaps

0

5

Local Similarity nes 3; Conserv

Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

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RESULT 29
AAP34656/c
ID AAP346
XX AAP346
XX Yeast;
XX Yeast;
XX Yeast;
XX NOT PI
XX HOCOOO
XX Linker
XX Li
                                                            The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not C coding sequence of a yeast gene selected from a group of 745 NORF (not C) previously assigned open reading frame; or nonannotated ORP) genes CC comprising a SAGE (serial analysis of gene expression) tag. Also CC (comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log CC phase, S phase and G2/M; (2) a method (M2) for screening candidate CC cell; and (b) monitoring expression of a NORF gene whose expression of CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell yeast gene is a candidate antifungal drug; (3) a method (M3) for CC comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression of CC contiguous nucleotides of a NORF gene whose expression varies as in M1; CC and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a CC yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene may be used to study, monitor and affect phases of the cell cycle, the differentially cycle and for identifycation of the cell cycle, the differentially cycle and for identification of the cell cycle. The CC expressed genes may be used as markers of phases of the cell cycle. The coll cycle and for identify candidate drugs which affect the cell cycle and the cycle and for identify candidate drugs. AAF3326 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-061874/07.
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10

: | | : | : : : 3

Matches

Conservative

Mismatches

<u>,</u>

Indels

0

Gaps

0

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RESULT 30

AAP43668

ID AAP43

XX AAP43

XX AAP43

XX Yeast

XX Ilike

OS Sacch

XX Ilike

OS Sacch

XX Ilike

OS Sacch

XX PO200

XX Ilike

PF 14-JU

XX Ilike

PF 14-JU

XX Ilike

PF 14-JU

XX Ilike

PF 14-JU

XX Yeast

PF 14-JU

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                                                                                          The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not comprising a ssigned open reading frame; or nonamnotated ORP) genes cc comprising a sAGE (serial analysis of gene expression) tag. Also comprising a SAGE (serial analysis of gene expression) tag. Also cc described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cleast 10% between any two phases of the cell cycle selected from log cp phase, S phase and G2/M; (2) a method (M2) for screening candidate cantifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a comprising contacting a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and contacting a spense candidate drug as a member of a cyeast cell comprising contacting a yeast cell with a candidate drug and contacting expression in a gene expression in a cyeast cell of a tleast 1 NORF gene whose expression in a cyeast cell of a tleast 1 NORF gene whose candidate drug and contacting a process of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The Cc methods may be used in the exemplification of the present invention. Cc AAF33267 represent SAGE to AAF33267 represent invention.
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Sequence 10 BP; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 371; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYJO ) UNIV JOHNS HOPKINS
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                                                                          exemplification of the present
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   A; 2 C;
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   G; 5 T; 0
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   U; 0 Other;
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Query Match
Best Local Similarity
 61.5%;
50.0%;
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15
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Sequence 10

BP;

4 A;

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RESULT 31 AAF40632/c ID AAF406 Coding sequence of a yeast gene selected from a group of 745 NORF (not comprising a SAGE (serial analysis of gene expression) tag. Also CC comprising a SAGE (serial analysis of gene expression) tag. Also CC described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at CC least 10% between any two phases of the cell cycle selected from log CC phase, S phase and G2/M; (2) a method (M2) for screening candidate CC cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 CC contiguous nucleotides of a NORF gene whose expression of CC contiguous nucleotides of a NORF gene whose expression varies as in M1; candidate cell comprising contacting a yeast cell with a condidate drug and CC waste cell comprising contacting a yeast cell with a candidate drug and CC contiguous nucleotides of a NORF gene whose expression varies as in M1; conditoring expression in the yeast cell of at least 1 NORF gene whose capression in a ffected by the class of drugs. The NORF gene whose correspondence of a conditoring expression in the yeast cell of at least 1 NORF gene whose capressed genes may be used as markers of phases of the cell cycle, the differentially capresent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention. 밁 Ś The present invention describes an isolated DNA molecule comprising coding sequence of a yeast gene selected from a group of 745 NORF ( AAF40632; Example; Page 263; 419pp; English. affecting phases of the cell Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and WPI; 2001-061874/07. Velculescu V, 14-JUN-2000; 2000WO-US016223 21-DEC-2000 WO200077214-A2. Saccharomyces cerevisiae. serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; one previously assigned open reading frame; nonannotated ORF; SAGE; Yeast NORF gene SAGE tag oligonucleotide 23-MAR-2001 (first entry AAF40632 standard; 16-JUN-1999; (UYJO ) UNIV JOHNS HOPKINS. N 6 UCUUUGCA 13 4; Vogelstein B, 9908-00335032 DNA; 10 4: cycle. Kinzler K; SEQ ID NO:7371

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RESULT 32
ACC69588/c
ID ACC695
XX ACC695
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XX Drosog
DT 16-JUL
XX Drosog
OS Drosog
OS Synthe
PN W0200:
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RESULT 33
AAD08670
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes the use of a cell, cell line or organism (collectively referred to as (I)) in which the activity of the Drosophila melanogaster gene cyp6g1, its derivatives or fragments, is increased relative to wild type activity of cyp6g1, for the screening of putative pesticides. Also described: (1) testing a putative pesticide for its potential resistance, by contacting (I) and detecting any detrimental effect on (I); (2) testing a putative pesticide for its potential resistance, by contacting (I) comprising a transposable element and detecting any detrimental effect on (I); and (3) a pesticide whose activity is detected by the above method; (I) is useful in the screening of putative pesticidees. The present sequence represents an oligonucleotide which flanks a 42 bp deletion of Drosophila melanogaster cyp6g1, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a cell, cell line or organism in which the activity of Drosophila melanogaster gene cyp6g1, is increased relative to wild type activity of cyp6g1, for the screening of putative pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster Synthetic.
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  AAD08670 standard; DNA; 9 BP.
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                                                                                                                                                                                                                                                                               DB 1;
15;
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Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter; HBV promoter; vancomycin-resistant enterococci promoter; VRB promoter; vanth promoter; androgen receptor promoter; AR promoter; human epidermal growth factor receptor 2 promoter; her2 promoter; beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer; colon cancer; immunological disorder; prostate cancer; cytostatic; autoimmune disease; HBV pre-S promoter; HBV-X promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer cells from mice. Cancer associated antigens and a pharmaceutical composition containing nucleic acid molecules encoding cancer associated antigens are used to treat a condition-e.g. cancer. Cancer associated antigens, the nucleotides encoding them, antibodies against them and the pharmaceutical compositions comprising them are useful for diagnosing, monitoring and treating the diseases characterised by the expression of one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for research purposes. Cancer associated antigens DNA is also useful in gene therapy. The present sequence is 5'RACE (rapid amplification of cDNA end) PCR primer used for isolating human full length OY-TES-1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to cancer associated antigens and their nucleic acids which are expressed in methylcholanthrene-induced fibrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide, useful in treating disorders such encoded by a nucleic acid (NA) Group 3 or 4 molecule.
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                                                                                                                                    Hepatitis B virus (HBV) domain 12-1 wild type
                                                                                                                                                                     23-APR-2002
                                                                                                                                                                                                      ABK29982;
                                                                                                                                                                                                                                     ABK29982 standard; DNA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9
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26-APR-2000; 2000US-00559013.
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                                                                                                                                                                                                                                                                                                                                                                                                      56.9%;
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Pred. No. 77;
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Search completed: September Job time: 0.001 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated nucleic acid regulatory sequence for CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci CC (VRE) promoter, an HBV promoter, vancomycin-resistant enterococci CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase CC (EBa) promoter. Transcription regulatory sequences may be used to CC regulate expression of the endogenous, autologous or heterologous genes CC operably linked to the promoter, and may be incorporated into CC transgenes. Regulated expression of cyclin D1 can be used in cancer CC therapies, such as breast, colon or pancreatic cancers and familial CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter CC may be used in the treatment of immunological disorders, such as a cutoimmune diseases e.g. multiple sclerosis (MS), systematic lupus CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid CC arthritis. Regulated expression of genes under the control of the HBV CC (hepatitis B) specific core, pre-S and X promoters can be used in the the control of the HBV CC (hepatitis B) specific core, pre-S and X promoters can be used in the patical promoter can be used in treatment of Enterococcus infection, while regulated expression of the vanH gene promoter can be used in treatment of Enterococcus infection, while regulated expression of the analyse receptor gene can be used in the treatment of prostate cof the invention to create mutant promoter fragments to determine the cof the invention.
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Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for recthe expression of transgenes and for treating e.g., cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard
Lim MY, Bruice TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8
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3; Conserva
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GTCTTTG 7
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42.9%;
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                                       2006, 12:04:34
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Maximum Match 100%
Listing first 17 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                        6.4
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seq length: 80
Unclassified.
1 (bases 1 to 13)
                                                                    Sequence 88 from patent US AR407995
                        Unknown
                                   Unknown.
                                                         AR407995.1
                                                                                           AR407995
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Gapop 10.0 , Gapext 0.5
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                                                         GI:40157982
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(c) 1993 - 2006 Biocceleration
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3.848 Million cell updates/sec
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AR303335
AX352859
AX301317
AX806339
CS071888
CCS133987
CQ766095
CQ766097
CQ766097
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ACCESSION: CS133987
ACCESSION: CQ766095
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ACCESSION:AR303335
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1:E02034
                                                                                                                                                                                                                        :AX104953
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                                                                                                                                                                                                                                                                      :CQ766097
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AX152859
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AR303335
AR303335.1
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Sequence 774 from Patent WO0138577.
AX152859
AX152859.1 GI:14534510
                                                                                                                                                             Homo sapiens (human)
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2 GICTIIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for synthesizing cDNA from mRNA sample Patent: US 6544736-A 60 08-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 10)
Shimamoto, A., Furuichi, Y., Shibata, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
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Fixing unit with an end imprint in a threaded terminal portion Patent: US 6632057-A 88 14-OCT-2003;

GPI Aerospace; Paris;
                                                Human transcriptomes
Patent: WO 0138577-A 774 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified
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                                                                                                  Velculescu, V.E., Vogelstein, B. and Kinzler, K.W
                                                                                                                           Hominidae; Homo.
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ilarity 53.8%;
Conservative (
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned RNA"
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50.0%;
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4; Mismatches
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Pred. No. 0.28;
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AX806339/c
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AX301317
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                                                  Local Similarity
 10
                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                     AX806339 10 bp 1
Sequence 20 from Patent W003025223.
AX806339
AX806339.1 GI:38523027
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                                                                                                                                                                              French-Constant,R.H. and Daborn,P.J.
Improvements in or relating to insecticide screening
Patent: WO 0302523-A 20 27-MAR-2003;
UNIVERSITY OF BATH (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31 from Patent W00185941. AX301317
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3; Conserv
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Academisch Ziekenhuis bij de Universiteit van Amsterdam
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                               organism="Drosophila melanogaster"
|mol_type="unassigned DNA"
|db_xref="taxon:727"
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                                                                                                   /note="Sequence flanking 42 bp deletion in
                                                                                                                                                                  Location/Qualifiers
  w
                                                            61.5%;
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37.5%;
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37.5%;
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                       RESULT 8
CQ766095/c
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CS133987/c
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CS071888
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Sequence
CQ766095
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                                                                                                                             9
                                                                                                                                                                                                                                                                                           Methods for synthesis of encoded libraries patent: WO 2005058479-A 529 30-JUN-2005; Praecis Pharmaceuticals Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                  synthetic construct synthetic construct
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Location/Qualifiers
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synthetic
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="synthetic construct"
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33.3%;
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Pred. No. 12;
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PAT 23-NOV-2004

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CQ766096/c
                                               PEATURES
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CQ766096
CQ766096.1
                                                                                                                                                                7 bp DNA
Sequence 58 from Patent WO2004005547.
CQ766097.1 GI:44908357
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3; Conserve
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IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
Location/Qualifiers
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                                                          Patent: WO 2004005547-A 58 15-JAN-2004; IMPERIAL COLLEGE INNOVATIONS LIMITED (G
                                                                                    Method
                                                                                                Weinzierl,R.
                                                                                                                        other sequences; artificial sequences.
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57 from Patent WO2004005547.
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="unassigned_DNA"
/mol_type="taxon:32630"
/mote="HS consensus sequence"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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         organism="synthetic construct"

mol_type="unassigned DNA"
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42.9%;
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CQ924619
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||:|:::
7 CGTCTTT 1
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CQ924619
CQ924619.1 GI:56214216
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Sakurai, T., Naruto, M. and Ozawa, H.
MANIFESTATION VECTOR FOR ANIMAL CELL
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             REFERENCES
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JP 1989196296-A/1.
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                                                                                                                                                                                                                                                                 other sequences; artificial sequences
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THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other sequences; artificial sequences.
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                                                                                                              08-AUG-1989
29-JAN-1988 JP 1988020174
SAKURAI TORU, NARUTO MASANOBU,
C12N15/00;
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                                                                                                                                                               Artificial sequence; Genes. JP 1989196296-A/1
                                                                       topology: Linear; hypothetical: No;
                                                                                                  strandedness: Single;
                                                                                                                                                                                        Artificial gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="8mer labelled probe"
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/note="HS consensus sequence"
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/Codon_start=1.
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Pred. No.
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Pred. No. 13;
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Hutet, E., Albina, E., Arnauld, C., Cariolet, R., Jestin, A., Le, C.P.,
Madec, F., Mahe, D., Blanchard, P. and Truong, C.
Circovirus sequences related to piglet weight loss disease (pwd)
Patent: WO 9929871-A 33 17-UNN-1999;
HUTET EVELYNE (FR); ALBINA EMMANUS (FR); ARNAULD CLAIRE (FR);
CARIOLET ROLAND (FR); JESTIN ANDRE (FR); LE CANN PIERRE (FR); MADEC
PRANCOIS (FR); MAHE DOMINIQUE (FR); BLANCHARD PHILIPPE (FR); TRUONG
CATHERINE (FR); VETERINAIRES ET ALIMENTAIRES C (FR)
                                                                                                                    other sequences; artificial sequences.

1 (bases 1 to 8)

Krieg, A.M., Schetter, C. and Vollmer, J.C.

Immunostimulatory nucleic acids

Patent: WO 0122972-A 1145 05-APR-2001;

UNIVERSITY OF IOWA RESEARCH FOUNDATION (
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AX104953.1 GI:13921150
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Viruses; ssDNA viruses; Circoviridae.
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AX003298
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                                        /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:39725"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Pred. No. 13;
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synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 8)
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                                                                                                                                                                                                                                                                                Genetic vaccine that mimics natural viral infection and induces long-lasting immunity to pathogens Patent: WO 0191536-A 3 06-DEC-2001;
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AX358376
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Plant internal ribosome entry segment
Patent: WO 0159138-A 21 16-AUG-2001;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
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AX211691
AX211691.1 GI:15523923
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/db_xref="taxon:32630"
/note="modified RNA editing site"
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/db_xref="taxon:32630"
/note="effector sequence"
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DEFINITION Sequence 5 from Patent WOO191536.
ACCESSION AX358378.1 GI:18675014
VERSION AX358378.1 GI:18675014

KEYWORDS
SOURCE
Synthetic construct
OTRCANISM sequences; artificial sequences.

REFERENCE 1
REFERENCE 1
AUTHORS Genetic vaccine that mimics natural viral infection and induces
JOURNAL 2
Genetic vaccine that mimics natural viral infection and induces
Inc. (US)
Incation/Qualifiers
Inc. (US)
PEATURES 1. 8
SOURCE //mol_type="genomic DNA"
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Maximum Match 100%
Listing first 4 summaries
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                                                        CURRENT APPLICATION NUMBER: US/09/847,601B
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
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                                                                                                                                                                                                                                           Sequence 88, Application US/09847601B
Publication No. US2050096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA C.
APPLICANT: GRANT, MARIA DENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND FILE REFERENCE: 4300.014100
SOPTWARE: PatentIn version 3.2
SEQ ID NO 88
LENGTH: 13
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US-10-330-627-774
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Sequence 12, Appl
Sequence 774, App
Sequence 31, Appl
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GENERAL INFORMATION:
APPLICANT: Volculescu, Victor E.
APPLICANT: Victor E.
APPLICANT: Kinzler, Kenneth W
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 774
                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-774
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US-10-330-627-774
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**OFTWARE: PatentIn version 3.3
$.**O ID NO 12
**LENGTH: 10
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APPLICANT: Wilson, C Grant
TITLS OF INVENTION: SYSTEM AND METHOD FOR THE DETECTION OF ANALYTES
PILE REFERENCE: 5119-12901
CURRENT APPLICATION NUMBER: US/10/832,469
TURRENT FILING DATE: 2004-04-26
RIOR APPLICATION NUMBER: US 60/465,336
RIOR BILING DATE: 2003-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Board of Regents, The University of Texas Systems APPLICANT: Schmid, Matthew J APPLICANT: Wilson, C Grant
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ORGANISM: Homo sapiens
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                                                    Conservative
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RESULT 4

US-10-293-222-31

Sequence 31, Application US/10293222

; Publication No. US20040033932A1

; GENERAL INFORMATION:
    APPLICANT: Versteeg, Rogier
    APPLICANT: Caron, Hubertus N.

TITLE OF INVENTION: MYC targets
    FILE REFERENCE: 2183-580US

; CURRENT APPLICATION NUMBER: US/10/293,222

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: PCT/NLO1/00361

PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: PCT/NLO1/00361

PRIOR FILING DATE: 2000-05-21

PRIOR FILING DATE: 2000-05-21

PRIOR PILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 455

SOFTWARE: Patentin Ver. 2.1

; EROTH: 10

; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-293-222-31

Query Match
    Best Local Similarity 37.5%; Pred. No. 1.7;

Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps

Qy 3 UCGUCUUU 10

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Db 1 TCGTCTTT 8

Search completed: September 1, 2006, 12:06:55

Job time: 0.001 secs
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Contact: Nahm B.H.

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Post-processing: Minimum Match
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Perfect score:
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re greater than or equal to the score of the result being pr
is derived by analysis of the total score distribution.
                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clace; Ehrhartoideae; Oryzeae; Oryza.
Large-scale Sequencing Analysis 
Unpublished (2003)
               Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., I
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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NACL--08-007.gl Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-007, mRNA
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Alkharouf,N. Khan,R. and Matthews,B.
Analysis of expressed sequence tags fi
infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alkharouf, N.W.
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1: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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Location/Qualifiers
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with_oligoribonucleotides and then used as templates
                                                                    /tissue_type="Roots"
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/clone lib="cDNA peking library 5, 4 day SCN3"
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/clone_lib="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was cap
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was cap
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/clone="NACL--08-007"
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HF500_42_54TR H
HF500_10-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: PMRichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawail) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 500 m Temperature: 7.25 C
Salinity: 34.07 psu Oxygen: 118.0 umol/kg
Class: fosmid ends.
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 CL658581
PRI0131d_E08 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science (2006) In press
Contact: Susan Lucas, Alex Copeland,
Kerrie Barry, Tijana Glavinadelrio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comparative genomics reveals ecological trends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Karl, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J., Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uncultured marine microorganism HF500 10-06-02 uncultured marine microorganism HF500 10-06-02 unclassified sequences; environmental samples.

1 (bases 1 to 6)
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/clone lib="HF500 10-06-02"

/clone lib="HF500 10-06-02"

/note="Vector: pcClFOS; North Pacific Subtropical Gyre

from marine picoplankton in the less than 1.6 um, greater

than 0.22 um fraction. Picoplankton collected at 500 m

depth on 10/6/2002, Coordinates: 22.45 N, 158 W Depth 500 m

Temperature: 7.25 C Salinity: 34.07 psu Oxygen: 118.0
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ll_type="marine picoplankton,
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xref="taxon:361149"
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Query Match
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AppaDB: an AcedB database
Pristionchus pacificus
Nucleic Acids Res. 32 (1),
                                                                                                                                                                                                                                   Srinivasan, J., Otto, G.W., AppaDB: an AcedB database
                                                                                                                                                                                                                                                                                        Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                              survey sequence.
CL667999
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
                                                                                             Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
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CL658581
This library was generated at sequenced at Vancouver, Canada
                Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
                                                                                                                                                        Contact: Sommer RJ
                                                                                                                                                                                            Pristionchus pacificus
Nucleic Acids Res. 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Sommer RJ
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Neodiplogasteridae; Pristionchus.
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/mol_type="genomic_DNA"
/strain="California"
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                                                                                                                                                                                              D421-D422 (2004)
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                                                                                                                                                                                                                                 U., Geisler,R. and Sommer,R.J. nematode satellite organism
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                    Pasadena,
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AppaDB: an AcedB database
Pristionchus pacificus
Nucleic Acids Res. 32 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS.
                                                                                                                                                                                                                                                                                                             Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                 Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa; Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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CL685291.1 GI:50193442
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PRI0140d_C11_2 - PRI0140d.
pacificus var. California
DU643362
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2; Conserv
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/mol_type="genomic DNA"
/strain="California"
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                                                                                                                                                                                 var. California"
                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                          db xref="taxon:54126"
clone_lib="Mixed stage fosmid library of
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25.0%;
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d.BR (5) Mixed
a Pristionchus
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Mainman,
Hominidae; Homo.

3 1 (bases 1 to 5)

S Ciuffi, A., Llano, M., Poeschla, E., Hoffmann, C., Leipzig, J.,
Shinn, P., Ecker, J.R. and Bushman, F.D.
A role for LEDGF/p75 in targeting HIV DNA integration
L Nat. Med. (2005) In press
Contact: Bushman FD
Department of Microbiology
University of Pennsylvania School of Medicine
University of Pennsylvania School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DU643819 5 bp DNA linear GS: Ciuffi-HIV-293T-wt-2-IIIC2.M13F Human Integration Site Library-Ciuffi-HIV-293t-wt Homo sapiens genomic, genom
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Ciuffi,A., Llano,M., Poeschla,B., H
Shinn,P., Ecker,J.R. and Bushman,F.
A role for LEDGF/p75 in targeting H
Nat. Med. (2005) In press
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Tel: 215 573 8732
Fax: 215 573 4856
Email: bushman@mail.med.upenn.edu
The hg17 (May 2004) freeze of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bushman@mail.med.upenn.edu
The hg17 (May 2004) freeze of the
Class: shotgun.
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University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
19104-6076, USA
                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Fax: 215 573 4856
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell type="293T"
/clone lib="Human Integration Site
Library-Ciuffi-HIV-293t-wt"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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  human genome was used.
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HIV DNA integration
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Local Similarity 50.0%;
hes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB093N19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 5)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
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DX081067
DX081067.1 GI:84775363
GSS.
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KBrB093N19R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB093N19, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Beom-Seok Park
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                                                                               Conservative
                                                                                                                                                   /lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic_DNA"
/mol_type="genomic_DNA"
/db_xref="taxon:9606"
/cell_type="293T"
/cell_type="293T"
/clone_lib="Human Integration Site
/clone_lib="Human Y-293t-wt"
                                                                                                                                                                                                                                                                                                          /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiitu"
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                                                                                                                                                                                                                                                  /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB093N19"
                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
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                                                                                               30.8%;
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Pred. No. 0;
2; Mismatches
                                                                           Score 4; DB 1; Length 5;
Pred. No. 0;
2; Mismatches 0; Indel
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Search completed: September 1, 2006, 12:07:57 Job time: 0.001 secs

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Result
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Maximum DB
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                                                 Sequence 88, Application US/09874601

Patent No. 6632057

Patent No. 6632057

PATENTAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
APPLICANT: GRANT, MARIA B.
APPLICANT: GRANT, MARIA B.
APPLICANTION: THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100

CURRENT APPLICATION NUMBER: US/09/874,601

CURRENT APPLICATION NUMBER: 09/063,667

PRIOR APPLICATION NUMBER: 09/063,667

PRIOR APPLICATION NUMBER: 60/046,147

PRIOR PILLING DATE: 1997-05-09

PRIOR FILING DATE: 1997-05-09

PRIOR FILING DATE: 1997-05-09

PRIOR FILING DATE: 1997-05-09
                   PRIOR APPLICATION NUMBER: 60/044,492 PRIOR FILING DATE: 1997-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 5
seq length: 80
SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0
61.5
49.2
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49.2
49.2
46.2
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1.820 Million cell updates/sec
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US-09-508-7538-60
US-09-585-599A-3
US-09-585-599A-5
US-09-514-245-45
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US-10-327-294-5
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Sequence 6, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 45, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
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              TYPE: RNA
ORGANISM: Artificial sequence
    FEATURE:
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-88
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                                                                                                       Sequence 3, Application US/09585599A
Patent No. 6544780
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES
TITLE OF INVENTION: LASTING IMMUNITY TO PATHOGENS
FILE REFERENCE: 22488-706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 472
SEQ ID NO 60
LENGTH: 10
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SEQ ID NO 3
LENGTH: 8
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Best Local (
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                                  CURRENT APPLICATION NUMBER: US/09/585,599A
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Biji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing
FILE REFERENCE: 00162/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: YUKO SHIBATA
APPLICANT: Hiroko FUNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Primer
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Pred. No.
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; TYPE: DNA
; ORGANISM: Type A PWD
US-09-514-245-45
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                                                                                                  SOFTWARE:
SEQ ID NO 45
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 2
                                                                                                                                                                                                                                              APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRU
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/09514245 Patent No. 6703023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/585,599A
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WANG, DANHER
APPLICANT: WANG, DANHER
TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES
TITLE OF INVENTION: LASTING IMMUNITY TO PATHOGENS
FILE REFERENCE: 22488-706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09585599A Patent No. 6544780
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Best Local (
                                                                                                                                                            FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
                                                                                                                                PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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2; Conserv
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BLANCHARD, Phillipe
HUTET, Evelyne
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                                                                    circovirus
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 49.2%;
37.5%;
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 Score 6.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0
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; OTHER INFORMATION: DNA of modified RNA editing site US-10-327-294-5
RESULT 8
US-09-432-020B-43/c
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US-10-327-294-5/c
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US-10-327-294-3
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                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wang, Danher
APPLICANT: Wang, Danher
TITLE OF INVENTION: COMPOSITION AND METHOD FOR STIMULATING IMMUNE RESPONSE TO PATHOGEN
TITLE OF INVENTION: COMPLEX ADENOVIRAL VECTOR
FILE REFERENCE: 22488-748
CURRENT APPLICATION NUMBER: US/10/327,294
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 8
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10327294
Patent No. 6964762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: COMPOSITION AND METHOD FOR STIMULATING IMMUNE RESPONSE TO PATHOGEN
TITLE OF INVENTION: COMPLEX ADENOVIRAL VECTOR
                                                                                                                                       Matches
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Patent No. 6964762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 22488-748
CURRENT APPLICATION NUMBER: US/10/327,294
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                            ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                              TYPE: DNA
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Pred. No. 0;
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Sequence 43, Application US/09432020B;
Patent No. 6288147;
GENERAL INFORMATION:
APPLICANT: Beattie, Kenneth Loren
ITILE OF INVENTION: Mucleic Acid Analysis Using Sequence-Targeted;
ITILE OF INVENTION: Tandem Hybridization
PILE REFERENCE: D6138
CURRENT APPLICATION NUMBER: US/09/432,020B;
CURRENT PILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: US 60/106,655
PRIOR APPLICATION NUMBER: US 60/106,655
PRIOR PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 55
SEQ ID NO 43
LENGTH: 7
TYPE: DNA
ORGANISM: artificial sequence
PEATURE: UFFORMATION: CF198 probe; the 3'terminal cytidine contains
OTHER INFORMATION: an aminopropanol which covalently binds to
OTHER INFORMATION: the epoxysilanized glass
US-09-432-020B-43
Query Match
Best Local Similarity 50.0%; Pred. No. 0;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps
Oy
Matches 3; Conservative 3; Mismatches 0; Gaps 0;
Matches 6; CGTCTT 1

Search completed: September 1, 2006, 12:05:44

Job time: 0.001 secs
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